**Fig. 1**

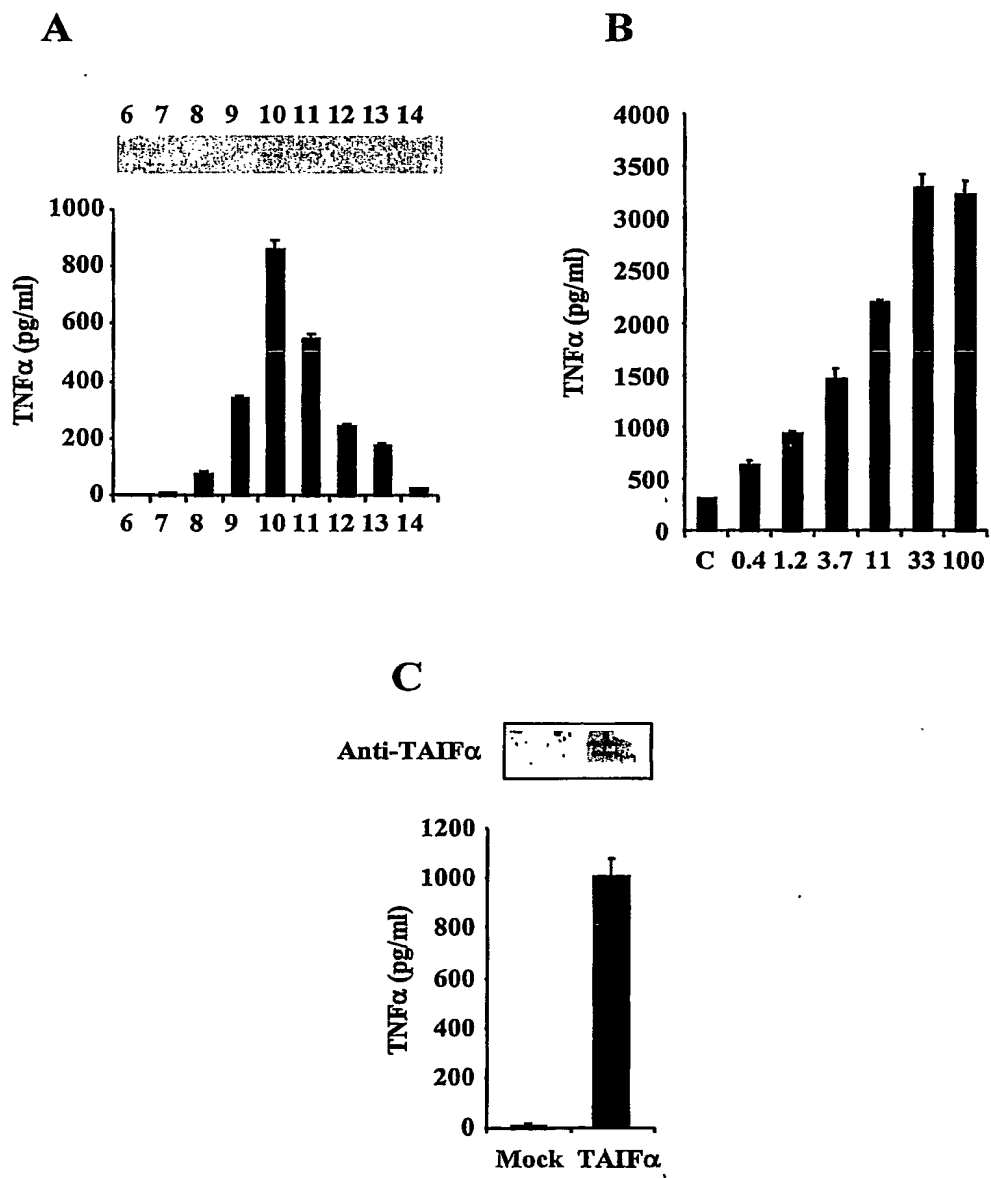


Fig. 2

IL-32 α	ATGTGCTTCCCGAAGGTCCTCTCTGATGACATGAAGAAGCTGAAGGCCCGAATG-----
IL-32 β	ATGTGCTTCCCGAAGGTCCTCTCTGATGACATGAAGAAGCTGAAGGCCCGAATG-----
IL-32 γ	ATGTGCTTCCCGAAGGTCCTCTCTGATGACATGAAGAAGCTGAAGGCCCGAATGGTAATG
IL-32 δ	-----ATGAAGAAGCTGAAGGCCCGAATG-----
IL-32 α	-----
IL-32 β	-----
IL-32 γ	CTCCTCCCTACTTCTGCTCAGGGGTTGGGGGCCTGGGTCTCAGCGTGTGACACTGAGGAC
IL-32 δ	-----
IL-32 α	-----
IL-32 β	-----
IL-32 γ	ACTGTGGGACACCTGGGACCCTGGAGGGACAAGGATCCGGCCCTTTGGTGCCAACTCTGC
IL-32 δ	-----
IL-32 α	-----CACCAGGCTATAGAAAGATTTTATGATAAAATGCAAAATGCAGAAATCA
IL-32 β	-----CACCAGGCCATAGAAAGATTTTATGATAAAATGCAAAATGCAGAAATCA
IL-32 γ	CTCTCTTCACAGCACCAGGCCATAGAAAGATTTTATGATAAAATGCAAAATGCAGAAATCA
IL-32 δ	-----CACCAGGCCATAGAAAGATTTTATGATAAAATGCAAAATGCAGAAATCA
IL-32 α	GGACGTGGACAGGTGATGTGCGAGCCTGGCAGAGCTGGAGGACGACTTCAAAGAGGGCTAC
IL-32 β	GGACGTGGACAGGTGATGTGCGAGCCTGGCAGAGCTGGAGGACGACTTCAAAGAGGGCTAC
IL-32 γ	GGACGTGGACAGGTGATGTGCGAGCCTGGCAGAGCTGGAGGACGACTTCAAAGAGGGCTAC
IL-32 δ	GGACGTGGACAGGTGATGTGCGAGCCTGGCAGAGCTGGAGGACGACTTCAAAGAGGGCTAC
IL-32 α	CTGGAGACAGTGGCGGCTTATTATGAGGAGCAGCACCCAGAGCTCACTCCTCTACTTGAA
IL-32 β	CTGGAGACAGTGGCGGCTTATTATGAGGAGCAGCACCCAGAGCTCACTCCTCTACTTGAA
IL-32 γ	CTGGAGACAGTGGCGGCTTATTATGAGGAGCAGCACCCAGAGCTCACTCCTCTACTTGAA
IL-32 δ	CTGGAGACAGTGGCGGCTTATTATGAGGAGCAGCACCCAGAGCTCACTCCTCTACTTGAA

Fig. 3A

IL-32 α	AAAGAAAGAGATGGATTACGGTGCCGAGGCAACAGATCCCCCTGTCCCGGATGTTGAGGAT
IL-32 β	AAAGAAAGAGATGGATTACGGTGCCGAGGCAACAGATCCCCCTGTCCCGGATGTTGAGGAT
IL-32 γ	AAAGAAAGAGATGGATTACGGTGCCGAGGCAACAGATCCCCCTGTCCCGGATGTTGAGGAT
IL-32 δ	AAAGAAAGAGATGGATTACGGTGCCGAGGCAACAGATCCCCCTGTCCCGGATGTTGAGGAT
IL-32 α	CCCGCAACCGAGGAGCCTGGGGAGAGCTTTTGTGACAAG-----
IL-32 β	CCCGCAACCGAGGAGCCTGGGGAGAGCTTTTGTGACAAGGTCATGAGATGGTTCCAGGCC
IL-32 γ	CCCGCAACCGAGGAGCCTGGGGAGAGCTTTTGTGACAAGGTCATGAGATGGTTCCAGGCC
IL-32 δ	CCCGCAACCGAGGAGCCTGGGGAGAGCTTTTGTGACAAGGTCATGAGATGGTTCCAGGCC
IL-32 α	-----
IL-32 β	ATGCTGCAGCGGCTGCAGACCTGGTGGCACGGGGTTCTGGCCTGGGTGAAGGAGAAGGTG
IL-32 γ	ATGCTGCAGCGGCTGCAGACCTGGTGGCACGGGGTTCTGGCCTGGGTGAAGGAGAAGGTG
IL-32 δ	ATGCTGCAGCGGCTGCAGACCTGGTGGCACGGGGTTCTGGCCTGGGTGAAGGAGAAGGTG
IL-32 α	-----
IL-32 β	GTGGCCCTGGTCCATGCAGTGCAGGCCCTCTGGAAACAGTTCCAGAGTTTCTGCTGCTCT
IL-32 γ	GTGGCCCTGGTCCATGCAGTGCAGGCCCTCTGGAAACAGTTCCAGAGTTTCTGCTGCTCT
IL-32 δ	GTGGCCCTGGTCCATGCAGTGCAGGCCCTCTGGAAACAGTTCCAGAGTTTCTGCTGCTCT
IL-32 α	-----TCCTACGGAGCCCCACGGGGGGACAAGGAG
IL-32 β	CTGTCAGAGCTCTTCATGTCCTCTTTCCAGTCCTACGGAGCCCCACGGGGGGACAAGGAG
IL-32 γ	CTGTCAGAGCTCTTCATGTCCTCTTTCCAGTCCTACGGAGCCCCACGGGGGGACAAGGAG
IL-32 δ	CTGTCAGAGCTCTTCATGTCCTCTTTCCAGTCCTACGGAGCCCCACGGGGGGACAAGGAG
IL-32 α	GAGCTGACACCCCAGAAGTGCTCTGAACCCCAATCCTCAAAAATGA
IL-32 β	GAGCTGACACCCCAGAAGTGCTCTGAACCCCAATCCTCAAAAATGA
IL-32 γ	GAGCTGACACCCCAGAAGTGCTCTGAACCCCAATCCTCAAAAATGA
IL-32 δ	GAGCTGACACCCCAGAAGTGCTCTGAACCCCAATCCTCAAAAATGA

Fig. 3B

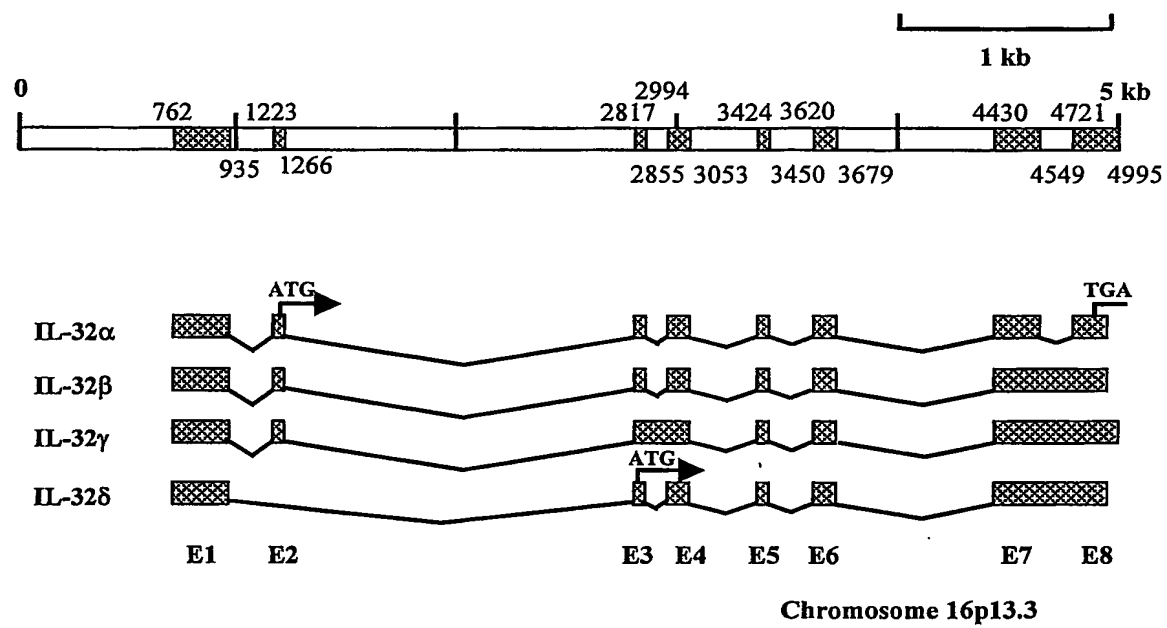
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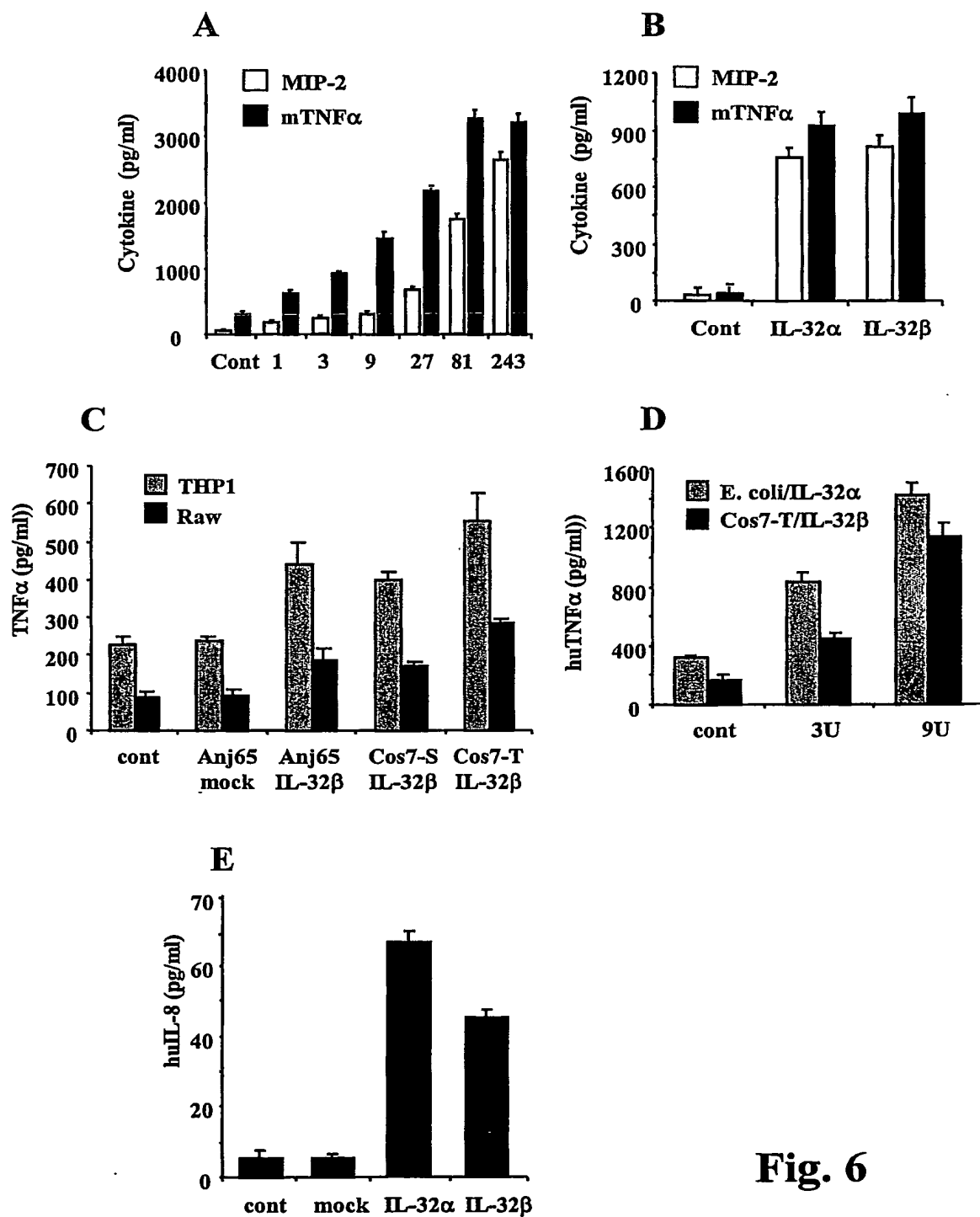
	1	Myr
IL-32 α	MCFPKVLSDDMKKLKARM-----	
IL-32 β	MCFPKVLSDDMKKLKARM-----	
IL-32 γ	MCFPKVLSDDMKKLKARMVMLLPTSAQGLGAWVSACDTEDTVGHLPWRDKDPALWCQLC	
IL-32 δ	-----MKKLKARM-----	
	61	Myr
IL-32 α	----HQAIERFYDKMQNAESGRGQVMSSLALEDDDFKEGYLETVAAYYEEQHPELTPLLE	
IL-32 β	----HQAIERFYDKMQNAESGRGQVMSSLALEDDDFKEGYLETVAAYYEEQHPELTPLLE	
IL-32 γ	LSSQHQAIERFYDKMQNAESGRGQVMSSLALEDDDFKEGYLETVAAYYEEQHPELTPLLE	
IL-32 δ	----HQAIERFYDKMQNAESGRGQVMSSLALEDDDFKEGYLETVAAYYEEQHPELTPLLE	
	121	Gly
IL-32 α	KERDGLRCRGNRSPVPDVEDPATEEPGESFCDK-----	
IL-32 β	KERDGLRCRGNRSPVPDVEDPATEEPGESFCDKVMRWFQAMLQRLQTWWHGVLAUVKEKV	
IL-32 γ	KERDGLRCRGNRSPVPDVEDPATEEPGESFCDKVMRWFQAMLQRLQTWWHGVLAUVKEKV	
IL-32 δ	KERDGLRCRGNRSPVPDVEDPATEEPGESFCDKVMRWFQAMLQRLQTWWHGVLAUVKEKV	
	181	Myr
IL-32 α	-----SYGAPRGDKHEELTPQKCSEPQSSK	
IL-32 β	VALVHAVQALWKQFQSFCCSLSELFMSFQSYGAPRGDKHEELTPQKCSEPQSSK	
IL-32 γ	VALVHAVQALWKQFQSFCCSLSELFMSFQSYGAPRGDKHEELTPQKCSEPQSSK	
IL-32 δ	VALVHAVQALWKQFQSFCCSLSELFMSFQSYGAPRGDKHEELTPQKCSEPQSSK	

B

	1
huIL-32 β	MCFPKVLSDDMKKLKARMHQAIERFYDKMQNAESGRGQVMSSLALEDDDFKEGYLETVAA
EqIL-32	MGYPKTSREDNERWKIRFHSTLDRWLDDIEVQSQGEEQVDLGLEDLEEKFSENILDAVEE
BoIL-32	MCFAKGVPPYDQASLRSIMHKRVDDFCDKMGNEPE-EAQMEAALDETEEGLSEDICEFIED
Consensus	*-----*-----*-----*-----*-----*-----*
	61
huIL-32 β	YYEEQHPELTPLLEKERDGLRCRGNRSPV----PDVEDP----ATE--EPGESFCDKVMR
EqIL-32	HHQKNNSSESAPLLPDVKPRLRRRAQKSSVLNPEPEPGPGILQVEALEAPEPEESFWVRAWR
BoIL-32	HIQENLPES--LQESSPL-LQEARQGVRRRIQRPSV----SARLEVQNPEESI---WA
Consensus	-----*-----*-----*-----*-----*-----*-----*
	121
huIL-32 β	WFQAMLQR-L-QTWWHGVLAUVKEKVVA-----LVHAVQALWKQFQS---FCCSLSELF
EqIL-32	SFMGMLQR-LKQRWQAVLA-WVREKVAAGWQA--LCSVAQSINSVLES---FCSYAGLF
BoIL-32	RALGRFQVIL-QSLQQR--WDALTWLREKAVTFLEAICSVVKAVLGVLTDFCSSVGQLF
Consensus	-----*-----*-----*-----*-----*-----*-----*
	181
huIL-32 β	MSSF---QSYGAPRGDKHEELTPQKCSEPQSSK
EqIL-32	RYH---IQV-----
BoIL-32	---GNLIQV-----
Consensus	-----*-----

Fig. 4

**Fig. 5**

**Fig. 6**

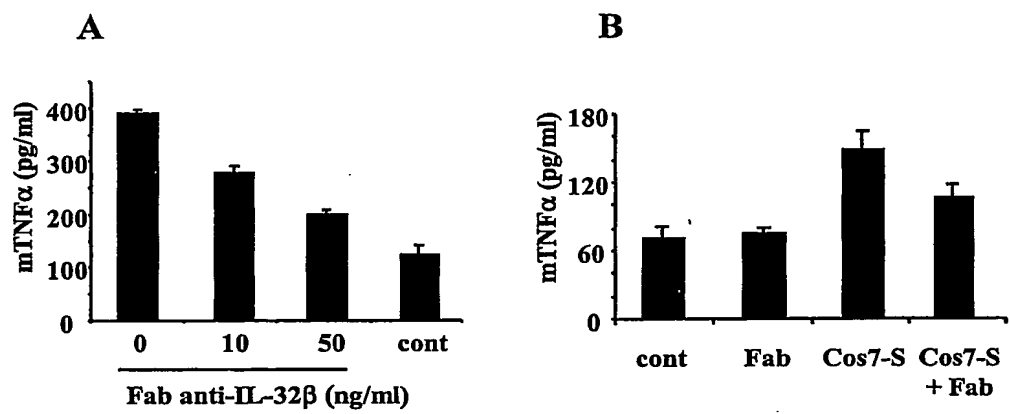
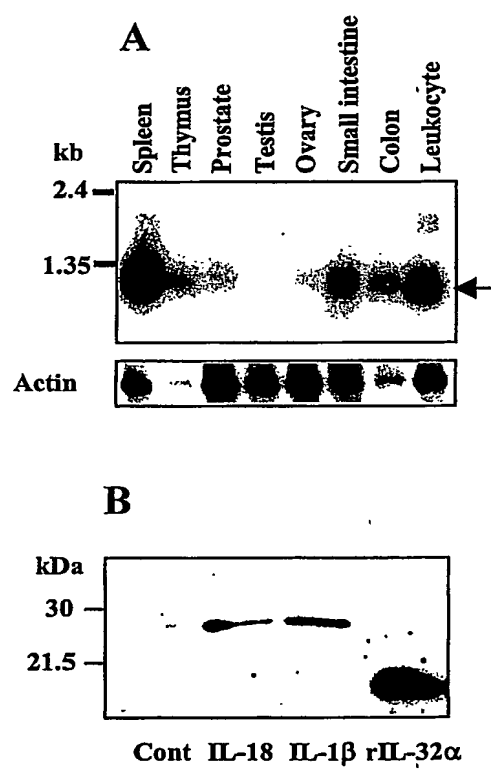
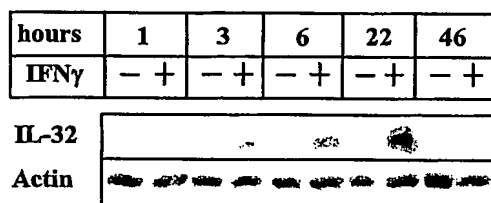
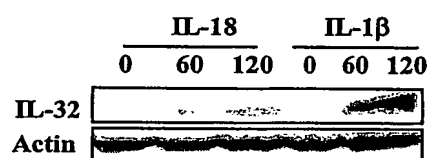
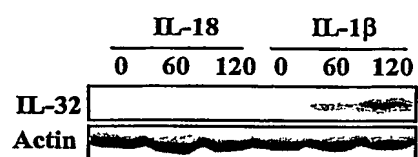
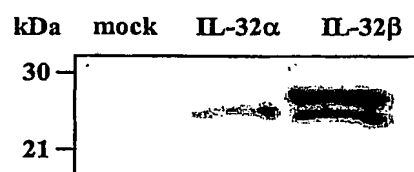
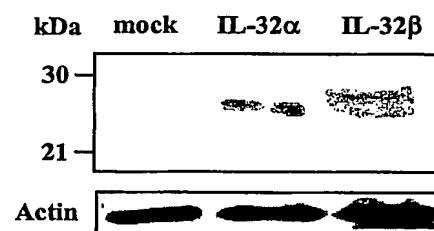
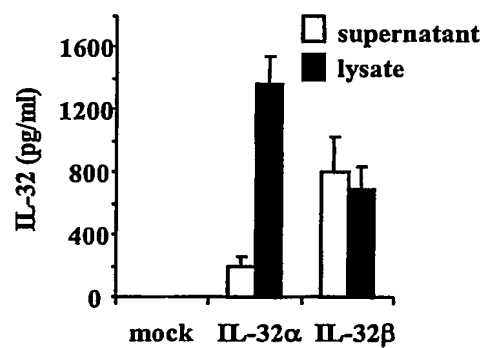
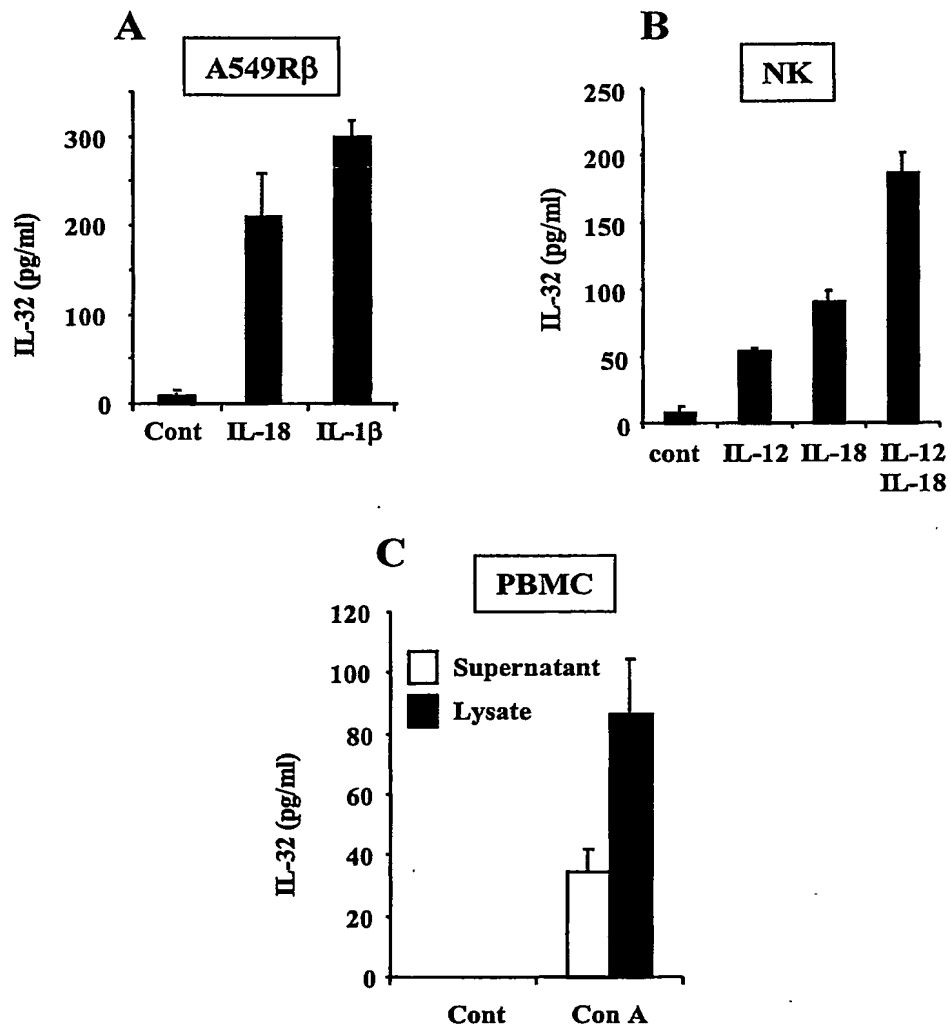


Fig. 7

**Fig. 8**

A**B****C****D****E****F****Fig. 9**

**Fig. 10**

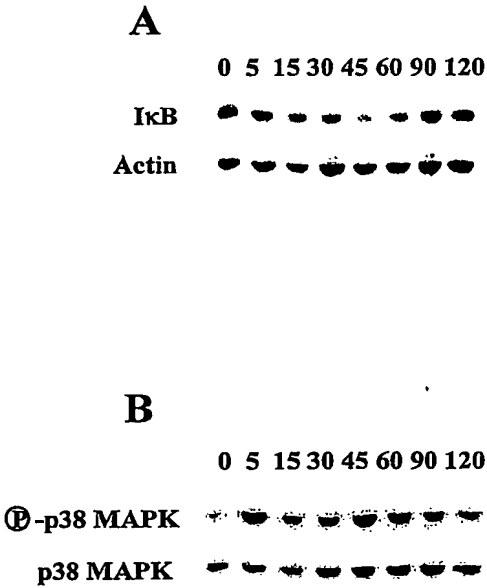


Fig. 11

MGYPKTSREDNERWKIRFHSTLDRWLDDIEVQSQGEEQVCQCAPTPCSRNLGGRVVMTMRRKNVPPQVD
LGPLTSPFSORTFRSDLCHLPTLDLSLTSLTSLCTAWPPCPPCTSCSGFLLQV

GCACGAGCTCGTGCCGTGTGTGCTGAGAGGCCCTTGGGGCAGGCACAGCCCCCTGGAATCCTGAGCTGCCATG
GGCTACCCCAAGACGTCCAGAGAAGACAATGAACGTTGGAAGATCCGATTTCACAGCACTTTAGACCGGT
GGCTTGATGATATCGAAGTTCAATCCCAAGGAGAGGAACAGGTGTGTCA GTGTGCTCCACGCCCTGCTC
CCGTAACCTCGGGGGTCGGGTGGTCACGATGACGATGAGGAGGAAGAACGTGCCACCTCAGGTCGATTTA
GGCCCTTTGACGTCCCCCTTTTCACAGAGAACCCTTCAGAA GTGACCTTTGCCACCTGCCTACCTTGACC
TGTCTTGACCACCTCCCTCACCTCCTTGCTGTGACAGCCTGGCCACCCTGCCACCATGCACCTTCTTG
CTCAGGTTTCCTTCTGCAGGTCTGACTTGTGGCTCCAGCGCATATGTCTTAATAAAAGTTGTG

MGYPKTSREDNERWKIRFHSTLDRWLDDIEVQSQGEEQVDLGLEDLEEKFSENILDAVEEHHQKNNSESA
 PLLPDVKPRLRRRAQKSSVLNPEPEGGILQVEALEAPEPEESFVWRWRSFMGMLQRLKQRWQAVLAWV
 REKVAAGWQALCSVAQSINSVLESFCSYAGLFRYHIQV

CTGAGAGGCCCTTGGGGCAGGCACGCCCTGGAATCCTGAGCTGCCATGGGGCTACCCCAAGACGTCCAG
AGAAGACAATGAACGTTGGGAAGATCCGATTTACAGCACTTTAGACCGGTGGCTTGATGATATCGAAGTT
CAATCCCAAGGAGAGGAACAGGTCGATTTAGGCC'TAGAAGACCTGGAGGAAAAATT'CAGTGAAAACATT
TTGACGCCGTGGAGGAGCACCATCAGAAGAACTCAGAATCTGCGCCTTTACTTCCTGACGTGAAGCC
CAGGTTACGTCGAGAGCTCAGAAGTCCTCTGTCTCAACCCTGAACCTGAGGGTCCAGGGATCCTGCAA
GTTGAGGCTCTAGAGGCACCCGAGCCTGAAGAAAGCTTTTGGGTGAGGCATGGAGGTCGTTTATGGGGA
TGCTACAGCGACTGAAGCAGAGGTGGCAGGCTGTACTGGCCTGGGTGCGAGAGAAGGTGGCTGCTGGCTG
GCAGGCCCTATGCAGTGTGGCCAGTCCATTAATAGTGTGCTTGAGAGTTTCTGCTCCTATATGGCTGGG
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CTTTGACGTCCCCCTTTTACAGAGAACCTTCAGAAGTGACCTTTGCCACCTGCCTACCCTTGACCTGTC
CTTGACCACCTCCCTCACCTCCTTGCTGTGCACAGCCTGGCCACCCTGCCACCATGCACTTCCTGCTCA
GGTTTTCCTTCTGCAGGTCTGACTTGTGGCTCCAGCGCATAGTCTT

A**BoIL-32 beta (SEQ ID NO:17)**

MCFAKGVYPDQASLRSIMHKRVDDFCDKMGNEPEEAQMEAAALDETEEGLSEDI CEFIEDHIQENLPESLQ
ESSPLLQEARQGVRRRIQRPSVSARLEVQNPEESIWARALGRFQVILQSLQQRCDALTWLREKAVTFLE
AICSVVKAVLGVLTDFCSSVGQLFGNLIQV

B**BoIL-32 beta (SEQ ID NO:21)**

CGGATTCGCGGATGCTCAGCTGGAGCTCTGGCTGCAGGATCTCAGGTCCCTTCGGGAGGACCCTAAGCC
ACCATGTGCTTCGCTAAGGGAGTCCCATATGACCAGGCTTCTCTGAGGTCCATAATGCACAAACGGGTGG
ATGATTTCTGTGATAAGATGGGAAATGAACCAGAAGAAGCACAGATGGAGGCAGCCCTAGATGAGACGGA
GGAGGGACTCAGCGAGGACATCTGTGAATTCATAGAAGATCACATTCAGAGAACCTTCCCGAATCCCTG
CAGGAGTCCAGTCCCTTGCTTCAGGAAGCACGGCAAGGAGTACGCCGCAGAATCCAGAGACCTTCAGTCT
CTGCCCGTCTGGAGGTCCAGAATCCGGAAGAGAGCATCTGGGCCAGAGCCCTGGGGAGGTTCCAAGTAAT
TCTGCAGAGTCTCCAGCAGCGGTGTTGGGATGCGCTCACCTGGCTGCGGGAGAAGGCGGTGACCTTCCTG
GAGGCCATCTGCAGTGTGGTGAAGGCCGTCTTGGGAGTGCTGACGATTTCTGCTCCTCTGTGGGGCAGC
TCTTCGAAACCTCATCCAGGTCTAGGAGCCGCAGGTGGTTCTGGAGGAACCTCCTCATCTAGGAGGC
CCTGCACCATCCCTTCCCAGAAACCATCTTGTGAAGCGACCTTTGCACTCCTGCTCACCTTGACCCAT
CCTTTAACTGCCCTCACCTCCTGT

C**BoIL-32 gamma (SEQ ID NO:22)**

MCFTKRDPRLASFRVLMVRSSFPRIAGVREAWVLLGAEENILAHLGPSREKNRDSFTQVHLC SQHNLVD
EFFDTMENEPEGAQMEAVLAETKEKFIKDAFKVMDNHIQENSPETLKESPLLQEARQEVRCRIQRRSVS
TSLEVQNPEESIWARALRQFLGILQSFLSGCRDALTWLWEKAAACLQAICSAVEALWEVLTD FCSFVGQL
LCRSLIQV

D**BoIL-32 gamma (SEQ ID NO:23)**

CGGGATCTCAGCTGGAGCTCTGGCTGCAGGATCTCAGGTCCCAGCGGCAGGACCCTAAGCCACCATGTGC
TTCACTAAGAGAGACCCACGTGTCTGGCTTCTTTTCAGGGTGTTAATGGTAAGAAGCTCATTTCCACGTA
TAGCTGGGGTTTCGGGAGGCCTGGGTTCTGCTGGGTGAAGCTGAGAACATTCTGGCCCACTTGGGACCCAG
CAGGGAGAAGAACCAGATTCTTTTACTCAAGTCCATCTCTGTTACAGCACAAACCTTG TAGATGAATTT
TTCGATACAATGGAAAATGAACCAGAAGGAGCACAGATGGAGGCAGTCCTAGCAGAGACTAAGGAGAAAT
TCATCAAGGACGCCTTTAAAGTCATGGATAATCACATTCAAGAGAACAGTCCCGAAACCTGAAGGAGTC
CAGTCCCTTGCTTCAGGAAGCACGGCAAGAAGTACGCTGCAGAATCCAGAGACGCTCCGTCTCCACCTCT
CTGGAGGTCCAGAATCCGGAAGAGAGCATCTGGGCCAGAGCCCTGCGGCAGTTCTTGGGCATTCTGCAGA
GTTTCCTGTCCGGGTGTCGGGATGCGCTCACCTGGCTGTGGGAGAAGGCCGCGGCCTGCCTACAGGCCAT
CTGCAGTGCGGTGGAGGCCCTCTGGGAAGTGCTCACGGATTTCTGCTCCTTTGTTGGGCAGCTCTTATGC
AGAAGCCTCATCCAGGTCTAAGAGCCTCACATGGTTCTGGAGGAGCCCCACCTCATT CAGAAGGCCCTGT
ACGATGCCCTTCCCGGAAACCATCTTCTGAAGCGACCTTTACCCTCCTGCTCACCTTGACCCATCCTTT
AACTGCCCTCCCCTCCTGTCCTG

Fig. 13

A**OvIL-32 alpha (SEQ ID NO:24)**

MCFARGVPHDQASLRSM LHTWVDHVCDKMGNEPEEAQMEAAALAEEMEEELSKDVCE SWKITFKRTFPNPCR
SPVPCFRKRSKKYAAESRDPQSLPVWRTRNRKRASGPEPCGGSEVFCGVSGSGVAMY

B**OvIL-32 alpha (SEQ IDO:25)**

CTGCGGTACCGGTCCGGATTCCCGGGCGAGACAGTGCTCAGCTGGAGCTCTGGCTGCAGGATCTCAGATC
CCAGCCGGAGGACCCTAATCCACCATGTGCTTCGCTAGGGGAGTCCCACATGACCAGGCTTCTCTGAGGA
GCATGCTGCACACCTGGGTGGATCATGTCTGTGATAAGATGGGAAATGAACCAGAAGAAGCACAGATGGA
GGCAGCCCTAGCAGAGATGGAGGAGGAACTCAGCAAGGATGTCTGTGAATCATGGAAGATCACATTCAAG
AGAACCTTCCCGAATCCCTGCAGGAGTCCAGTCCCTTGCTTCAGGAAGCGCAGCAAGAAGTACGCCGCAG
AATCCAGAGACCCTCAGTCTCTGCCTGTCTGGAGGACCAGAAACCGGAAGAGAGCATCTGGGCCAGAGCC
CTGCGGCGGTTCCGAGGTTTTCTGCGGAGTCTCTGGCAGCGGTGTTGCGATGTACTGACCTGGCTGCAGG
AGAAGGCGGCGGCTGCCTGGAGGCCGTCTGCAGTGCGGTGAAGACCATCTGGGGAGTGCTGACGGATTT
CTGCTCCTCTGTGGGGCAGCTCTTCAGAAACCTCATCCAGGTCTAGGAGCCCCAGGTCGTTCTTGAGGAA
CTGCTCCTCATCTAGAAGGCCCTGCACAATCCCCTTCCCAGAAACCATCTTCTGAAGCGACCTTTACCCT
CCTGTTACCCTTCACCAATCCTTTAACTGCCCTCACCTCCTGTCTGCAGGGACGACACCACAACATCAA
GCCAGGTTTCCCTTCTCCAAGTCTGACCCGTCTGTCAGGGA

C**SwIL-32 alpha (SEQ ID NO:26)**

MRGVSATRTLPLKAGPQPRSG LGLPLPRRVPEPPPI PAESSPLLNEVRQGVRSRVRRPPGHNQPHYALAVR
EPRQSTFRRIELFEEM LKRLQQRWRGALAWVQERAAACFRGLCRALEAFWSLVQSFCSSMGHAFGSVIQ
V

D**SwIL-32 alpha (SEQ ID NO:27)**

ATGACTTGAGGGGAACTGAGCGGCCAGGCCAGCCCCTGGGAAAAGTCCTGGGGTCTGTGGGGCTGTTG
GCAGGAAAGCAGCCTGTGTCCAAGGCGGGGCATGAGGGGGGTGTCTGCCACCAGGACTCTCCCAAAGGCA
GGGCCTCAGCCAAGGTCAGGACTGGGGCTGCCTCTCCCAGGCGGGTCCCTGAACCACCCCCCATCCCTG
CAGAATCCAGTCCTCTGCTCAACGAAGTCCGGCAGGGAGTCCGTTCTAGAGTCCGAAGGCCTCCTGGCCA
CAACCAGCCACATTATGCGCTAGCGGTCCGGGAGCCCAGGCAGAGCACTTTCAGACGCATCCTTGAGCTG
TTTGAGGAAATGCTGAAGCGCCTGCAGCAGAGGTGGAGGGGTGCCCTGGCTTGGGTGCAGGAAAGGGCTG
CTGCCTGCTTCCGGGGCTTGTGCAGGGCCCTTGAAGCTTTCTGGAGCCTGGTGCAGAGTTTTTGCTCCTC
CATGGGGCAGCCTTCGGGAGTGTATCCAGGTCTAAGGTGCTCCAGGTGAAATAAGAGTTTCTAGAGCA
CAACCTCCCCCTGCCTTGGCTAAAAAGGCAGCTGTAAGCCTTT

Fig. 14

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